

FULL ESTIMATED COST

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0.21 0.21

FILE 'MEDLINE' ENTERED AT 12:34:45 ON 17 MAY 2006

FILE 'CAPLUS' ENTERED AT 12:34:45 ON 17 MAY 2006

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=> s (phosphodiesterase or pde4b or protein (w) kinase (3a) beta or pkc#)
L1 97084 (PHOSPHODIESTERASE OR PDE4B OR PROTEIN (W) KINASE (3A) BETA OR
PKC#)

=> s l1 and lymphoma
L2 635 L1 AND LYMPHOMA

=> s l2 and (correlat? or outcome# or treatment# or survival or rate#)
L3 303 L2 AND (CORRELAT? OR OUTCOME# OR TREATMENT# OR SURVIVAL OR RATE#
)

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4 223 DUP REM L3 (80 DUPLICATES REMOVED)

=> s l4 and express?
L5 111 L4 AND EXPRESS?

=> d 1-111 ti

L5 ANSWER 1 OF 111 MEDLINE on STN
TI Expression of PKC-beta or cyclin D2 predicts for
inferior survival in diffuse large B-cell lymphoma.

L5 ANSWER 2 OF 111 MEDLINE on STN
TI Splenic marginal zone lymphoma: proposal of new diagnostic and
prognostic markers identified after tissue and cDNA microarray analysis.

L5 ANSWER 3 OF 111 MEDLINE on STN
TI A hydrogen peroxide-generating agent, 6-formylpterin, enhances
heat-induced apoptosis.

L5 ANSWER 4 OF 111 MEDLINE on STN
TI Stimulation of CD95-induced apoptosis in T-cells by a subtype specific
neutral sphingomyelinase inhibitor.

L5 ANSWER 5 OF 111 MEDLINE on STN
TI The phosphodiesterase PDE4B limits cAMP-associated
PI3K/AKT-dependent apoptosis in diffuse large B-cell lymphoma.

L5 ANSWER 6 OF 111 MEDLINE on STN
TI RLIP76 (RALBP1)-mediated transport of leukotriene C4 (LTC4) in cancer
cells: implications in drug resistance.

L5 ANSWER 7 OF 111 MEDLINE on STN
TI Expression of DNA-PKcs and Ku86, but not Ku70, differs
between lymphoid malignancies.

L5 ANSWER 8 OF 111 MEDLINE on STN
TI Characterization of expression of protein kinase C isozymes in
human B-cell lymphoma: Relationship between its
expression and prognosis.

L5 ANSWER 9 OF 111 MEDLINE on STN
TI Integration of DAG signaling systems mediated by PKC-dependent
phosphorylation of RasGRP3.

L5 ANSWER 10 OF 111 MEDLINE on STN
TI Sialic acids linked to glycoconjugates of Fas regulate the

caspase-9-dependent and mitochondria-mediated pathway of Fas-induced apoptosis in Jurkat T cell lymphoma.

L5 ANSWER 11 OF 111 MEDLINE on STN

TI Effects of aminophylline on proliferation and apoptosis in Raji lympho-blastoid cell line.

L5 ANSWER 12 OF 111 MEDLINE on STN

TI Intercellular adhesion molecule-1 expression on human corneal epithelial outgrowth from limbal explant in culture.

L5 ANSWER 13 OF 111 MEDLINE on STN

TI Differential expression of protein kinase C isoenzymes related to high nitric oxide synthase activity in a T lymphoma cell line.

L5 ANSWER 14 OF 111 MEDLINE on STN

TI Interactions between 2-fluoroadenine 9-beta-D-arabinofuranoside and the kinase inhibitor UCN-01 in human leukemia and lymphoma cells.

L5 ANSWER 15 OF 111 MEDLINE on STN

TI Crucial importance of PKC-beta(I) in LFA-1-mediated locomotion of activated T cells.

L5 ANSWER 16 OF 111 MEDLINE on STN

TI Oligonucleotide sequence-specific inhibition of gene expression, tumor growth inhibition, and modulation of cAMP signaling by an RNA-DNA hybrid antisense targeted to protein kinase A RIalpha subunit.

L5 ANSWER 17 OF 111 MEDLINE on STN

TI Distinct molecular mechanisms of Fas resistance in murine B lymphoma cells.

L5 ANSWER 18 OF 111 MEDLINE on STN

TI Transforming growth factor beta 1 stimulates expression of the Epstein-Barr virus BZLF1 immediate-early gene product ZEBRA by an indirect mechanism which requires the MAPK kinase pathway.

L5 ANSWER 19 OF 111 MEDLINE on STN

TI Theophylline, pentostatin (Nipent), and chlorambucil: a dose-escalation study targeting intrinsic biologic resistance mechanisms in patients with relapsed lymphoproliferative disorders.

L5 ANSWER 20 OF 111 MEDLINE on STN

TI The cAMP signaling pathway as a therapeutic target in lymphoid malignancies.

L5 ANSWER 21 OF 111 MEDLINE on STN

TI Prostaglandin E2-induced up-regulation of c-fos messenger ribonucleic acid is primarily mediated by 3',5'-cyclic adenosine monophosphate in MC3T3-E1 osteoblasts.

L5 ANSWER 22 OF 111 MEDLINE on STN

TI Protein kinase C-alpha is essential for Ramos-BL B cell survival

.

L5 ANSWER 23 OF 111 MEDLINE on STN

TI CD27 signals through PKC in human B cell lymphomas.

L5 ANSWER 24 OF 111 MEDLINE on STN

TI The role of protein kinase C signaling in activated DRA transcription.

L5 ANSWER 25 OF 111 MEDLINE on STN

TI Stabilization of invariant chain mRNA by 12-O-tetradecanoylphorbol-13-acetate is blocked by IFN-gamma in a murine B lymphoma cell line.

L5 ANSWER 26 OF 111 MEDLINE on STN

TI DNA-PKcs: a T-cell tumour suppressor encoded at the mouse scid

locus.

- L5 ANSWER 27 OF 111 MEDLINE on STN
TI Calphostin C synergistically induces apoptosis with VP-16 in lymphoma cells which **express** abundant phosphorylated Bcl-2 protein.
- L5 ANSWER 28 OF 111 MEDLINE on STN
TI B cell receptor cross-linking prevents Fas-induced cell death by inactivating the IL-1 beta-converting enzyme protease and regulating Bcl-2/Bcl-x **expression**.
- L5 ANSWER 29 OF 111 MEDLINE on STN
TI Protein kinase C is required for induction of 2',5'-oligoadenylate synthetases.
- L5 ANSWER 30 OF 111 MEDLINE on STN
TI Pentoxyfylline promotes replication of human cytomegalovirus in vivo and in vitro.
- L5 ANSWER 31 OF 111 MEDLINE on STN
TI Cell-permeable ceramide inhibits the growth of B lymphoma Raji cells lacking TNF-alpha-receptors by inducing G0/G1 arrest but not apoptosis: a new model for dissecting cell-cycle arrest and apoptosis.
- L5 ANSWER 32 OF 111 MEDLINE on STN
TI Inhibitory effect of a synthetic prostacyclin analogue, beraprost, on urokinase-type plasminogen activator **expression** in RC-K8 human lymphoma cells.
- L5 ANSWER 33 OF 111 MEDLINE on STN
TI Protein kinase C-delta mRNA is down-regulated transcriptionally and post-transcriptionally by 12-O-tetradecanoylphorbol-13-acetate.
- L5 ANSWER 34 OF 111 MEDLINE on STN
TI Phorbol ester-stimulated phosphorylation of PU.1: association with leukemic cell growth inhibition.
- L5 ANSWER 35 OF 111 MEDLINE on STN
TI Activation of protein kinase Cdelta in human myeloid leukemia cells treated with 1-beta-D-arabinofuranosylcytosine.
- L5 ANSWER 36 OF 111 MEDLINE on STN
TI Isolation and characterization of cell lines with genetically distinct mutations downstream of protein kinase C that result in defective activation-dependent regulation of T cell integrin function.
- L5 ANSWER 37 OF 111 MEDLINE on STN
TI Phorbol ester stimulated cathepsin L **expression** in U937 cells.
- L5 ANSWER 38 OF 111 MEDLINE on STN
TI Invariant chain (CD74) gene regulation: enhanced **expression** associated with activation of protein kinase C delta in a murine B lymphoma cell line.
- L5 ANSWER 39 OF 111 MEDLINE on STN
TI Protein kinase C mediates activation of nuclear cAMP response element-binding protein (CREB) in B lymphocytes stimulated through surface Ig.
- L5 ANSWER 40 OF 111 MEDLINE on STN
TI Regulation of apoptosis induced by the retinoid N-(4-hydroxyphenyl) retinamide and effect of deregulated bcl-2.
- L5 ANSWER 41 OF 111 MEDLINE on STN
TI Growth of S49 wild type cells in 3 nM epinephrine increases cyclic AMP phosphodiesterase activity.
- L5 ANSWER 42 OF 111 MEDLINE on STN

- TI Modulation of human DNA methyltransferase activity and mRNA levels in the monoblast cell line U937 induced to differentiate with dibutyryl cyclic AMP and phorbol ester.
- L5 ANSWER 43 OF 111 MEDLINE on STN
TI Regulation of the BZLF1 promoter of Epstein-Barr virus by second messengers in anti-immunoglobulin-treated B cells.
- L5 ANSWER 44 OF 111 MEDLINE on STN
TI Conventional protein kinase C isoforms are not essential for cellular proliferation of a T cell lymphoma line.
- L5 ANSWER 45 OF 111 MEDLINE on STN
TI Regulation of protein kinase C isoform proteins in phorbol ester-stimulated Jurkat T lymphoma cells.
- L5 ANSWER 46 OF 111 MEDLINE on STN
TI Expression of nucleotide pyrophosphatase and alkaline phosphodiesterase I activities of PC-1, the murine plasma cell antigen.
- L5 ANSWER 47 OF 111 MEDLINE on STN
TI Second-messenger pathways involved in the regulation of survival in germinal-centre B cells and in Burkitt lymphoma lines.
- L5 ANSWER 48 OF 111 MEDLINE on STN
TI Prolactin-induced proliferation of the Nb2 T-lymphoma is associated with protein kinase-C-independent phosphorylation of stathmin.
- L5 ANSWER 49 OF 111 MEDLINE on STN
TI Transient down-regulation of PKC-zeta RNA following crosslinking of membrane IgM on WEHI-231 B lymphoma cells.
- L5 ANSWER 50 OF 111 MEDLINE on STN
TI Protein kinase C activation and protooncogene expression in differentiation/retrodifferentiation of human U-937 leukemia cells.
- L5 ANSWER 51 OF 111 MEDLINE on STN
TI The involvement of protein kinase C in mediating growth suppressive signals of interferons in hematopoietic cells.
- L5 ANSWER 52 OF 111 MEDLINE on STN
TI Regulation of leukocyte adhesion molecule-1 (TQ1, Leu-8) expression and shedding by normal and malignant cells.
- L5 ANSWER 53 OF 111 MEDLINE on STN
TI Modulation of IFN-mediated Ly-6E antigen induction by cAMP in a T cell lymphoma: opposite effects on the responses to IFN-gamma and IFN-alpha/beta.
- L5 ANSWER 54 OF 111 MEDLINE on STN
TI Transmembrane signalling associated with ganglioside-induced CD4 modulation.
- L5 ANSWER 55 OF 111 MEDLINE on STN
TI Conversion of high grade lymphoma tumor cell line to intermediate grade with TPA and bryostatin 1 as determined by polypeptide analysis on 2D gel electrophoresis.
- L5 ANSWER 56 OF 111 MEDLINE on STN
TI Mechanisms of degradation of 2'-5' oligoadenylates.
- L5 ANSWER 57 OF 111 MEDLINE on STN
TI Prolactin as a mammalian mitogen and tumor promoter.
- L5 ANSWER 58 OF 111 MEDLINE on STN
TI Early ionic events associated with phorbol ester induced differentiation and inhibition of cell growth in hematopoietic tumor cell lines.

- L5 ANSWER 59 OF 111 MEDLINE on STN
TI Role of high affinity cAMP phosphodiesterase activities in the response of S49 cells to agonists.
- L5 ANSWER 60 OF 111 MEDLINE on STN
TI Phorbol myristate acetate inhibits growth in S49 cells: isolation of resistant variants.
- L5 ANSWER 61 OF 111 MEDLINE on STN
TI Identification by direct photoaffinity labeling of an altered phosphodiesterase in a mutant S49 lymphoma cell.
- L5 ANSWER 62 OF 111 MEDLINE on STN
TI Effect of bleomycin on DNA, RNA, protein, chromatin and on cell transformation by oncogenic RNA viruses.
- L5 ANSWER 63 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Screening parkinson's disease therapeutics based on genes differentially expressed in A9 dopaminergic neurons
- L5 ANSWER 64 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profiles and predictive model for atherosclerosis and susceptibility to atherosclerosis
- L5 ANSWER 65 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profiling in the diagnosis of hematological malignancies
- L5 ANSWER 66 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Regulation of radiation-induced protein kinase C δ activation in radiation-induced apoptosis differs between radiosensitive and radioresistant mouse thymic lymphoma cell lines
- L5 ANSWER 67 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI 2-Amidothiazole-based compounds as inhibitors of ATP-utilizing enzymes, their preparation, pharmaceutical compositions, and use in therapy
- L5 ANSWER 68 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profiles for identifying patients at risk of developing encephalitis following immunotherapy for Alzheimer's disease
- L5 ANSWER 69 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profile for predicting activity of compounds that interact with and/or modulate protein tyrosine kinases and/or protein tyrosine pathways in lung cancer cells
- L5 ANSWER 70 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Role of MKK3 and p38 MAPK in cytokine-induced death of insulin-producing cells
- L5 ANSWER 71 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Differential expression of molecules associated with acute stroke
- L5 ANSWER 72 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI FLT3 internal tandem duplication mutations induce myeloproliferative or lymphoid disease in a transgenic mouse model
- L5 ANSWER 73 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Role of Bcl-2 in the arachidonate-mediated survival signaling preventing mitochondrial permeability transition-dependent U937 cell necrosis induced by peroxynitrite
- L5 ANSWER 74 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profiles in the diagnosis and treatment of Alzheimer's disease
- L5 ANSWER 75 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profile for determining graft tolerant phenotype

in a subject and for determination of an immunosuppressive therapy regimen

L5 ANSWER 76 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI The curcuminoids- and anthocyanins-responsive genes in human adipocytes and their use in screenings of anti-obesity and anti-diabetes drugs

L5 ANSWER 77 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Use of enzymatic inhibitors of h-PRUNE for the prevention and treatment of the metastases of tumours overexpressing h-PRUNE

L5 ANSWER 78 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Differentially expressed gene profile for diagnosing and treating mental disorders

L5 ANSWER 79 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Interleukin-12 (IL-12) induces T lymphocyte apoptosis and affects the expression and signal transduction of Bcl-2

L5 ANSWER 80 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Gene expression profile providing biomarkers for predicting the progression of colorectal adenocarcinoma

L5 ANSWER 81 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Biomarkers of cyclin-dependent kinase modulation in cancer therapy

L5 ANSWER 82 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Gene expression that correlated with breast cancer recurrence and patient survival, and diagnostic and therapeutic uses thereof

L5 ANSWER 83 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI DEF domain-containing members of the MAP kinase pathway and their use in screening for drug inhibitors

L5 ANSWER 84 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Gene expression profiles and biomarkers for the detection of Chagas disease and other disease-related gene transcripts in blood

L5 ANSWER 85 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Gene expression profiles and biomarkers for the detection of lung disease-related and other disease-related gene transcripts in blood

L5 ANSWER 86 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Sequences of human schizophrenia related genes and use for diagnosis, prognosis and therapy

L5 ANSWER 87 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Systems, methods and kits for characterizing phosphoproteomes by digestion, chromatography and mass spectrometry

L5 ANSWER 88 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Systems and methods for characterizing a biological condition or agent using calibrated gene expression profiles

L5 ANSWER 89 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Gene expression profiling for diagnosis and treatment of angiogenesis-related disorders

L5 ANSWER 90 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Inflammation-associated genes and proteins for assessing transplant recipient's risk of delayed graft function, graft rejection and long-term prognosis

L5 ANSWER 91 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

TI Purification, cloning and characterization of L-amino acid oxidase with cytotoxic activity from Aplysia punctata and use for the diagnosis and treatment of cancer

L5 ANSWER 92 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN

- TI Surrogate marker gene expression-based methods for identifying antineoplastic agents
- L5 ANSWER 93 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Human protein kinase C .beta. isoform sequence homologs (PRKCB1) as modifiers of the branching morphogenesis and use in cancer diagnosis, therapy and drug screening
- L5 ANSWER 94 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI CARD11 NF- κ B activating protein CARMA-1 as a central regulator of humoral immune responses and atopy and a cDNA encoding and their use in treatment of immune disorders
- L5 ANSWER 95 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Use of mouse genes involved in tumor development for the development of anti-cancer drugs
- L5 ANSWER 96 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Diffuse large cell lymphoma diagnosis and outcome prediction by gene expression analysis
- L5 ANSWER 97 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI IL-12 induces T lymphocytes apoptosis and influences the expression and signal transduction of Fas/FasL
- L5 ANSWER 98 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Activation of the Epstein-Barr virus lytic cycle by the latex of the plant Euphorbia tirucalli
- L5 ANSWER 99 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Nucleic acid and corresponding protein designated 161P2F10B useful in treatment and detection of cancer
- L5 ANSWER 100 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Antisense oligonucleotide inhibition of protein kinase C- α expression for treatment of
- L5 ANSWER 101 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Endocrine disruptor screening using DNA chips of endocrine disruptor-responsive genes
- L5 ANSWER 102 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Novel phosphodiesterases of trypanosomes and human with potential use as therapeutic targets and cDNAs encoding
- L5 ANSWER 103 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI DNA-PKcs mutations in dogs and horses: allele frequency and association with neoplasia
- L5 ANSWER 104 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Diffuse large B-cell lymphoma outcome prediction by gene-expression profiling and supervised machine learning
- L5 ANSWER 105 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Macrocylic diterpenes for treatment and prophylaxis of PKC-related conditions
- L5 ANSWER 106 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Investigation of differentially expressed genes during the development of mouse cerebellum
- L5 ANSWER 107 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Comparative genome-scale analysis of gene expression profiles in T cell lymphoma cells during malignant progression using a complementary DNA microarray
- L5 ANSWER 108 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI cDNA microarray gene expression analysis of B-cell chronic lymphocytic leukemia proposes potential new prognostic markers involved in

lymphocyte trafficking

L5 ANSWER 109 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Gene expression profiling of primary breast carcinomas using arrays of candidate genes

L5 ANSWER 110 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Antisense therapy of hematologic malignancies

L5 ANSWER 111 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Regulation of p21WAF1/CIP1 expression by p53-independent pathways

=> d 104, 107, 108, 109, 96, 88 bib ab

L5 ANSWER 104 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:33833 CAPLUS
DN 136:230307
TI Diffuse large B-cell lymphoma outcome prediction by gene-expression profiling and supervised machine learning
AU Shipp, Margaret A.; Ross, Ken N.; Tamayo, Pablo; Weng, Andrew P.; Kutok, Jeffery L.; Aguiar, Ricardo C. T.; Gaasenbeek, Michelle; Angelo, Michael; Reich, Michael; Pinkus, Geraldine S.; Ray, Tane S.; Koval, Margaret A.; Last, Kim W.; Norton, Andrew; Lister, T. Andrew; Mesirov, Jill; Neuberg, Donna S.; Lander, Eric S.; Aster, Jon C.; Golub, Todd R.
CS Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA
SO Nature Medicine (New York, NY, United States) (2002), 8(1), 68-74
CODEN: NAMEFI; ISSN: 1078-8956
PB Nature America Inc.
DT Journal
LA English
AB Diffuse large B-cell lymphoma (DLBCL), the most common lymphoid malignancy in adults, is curable in less than 50% of patients. Prognostic models based on pre-treatment characteristics, such as the International Prognostic Index (IPI), are currently used to predict outcome in DLBCL. However, clin. outcome models identify neither the mol. basis of clin. heterogeneity, nor specific therapeutic targets. We analyzed the expression of 6817 genes in diagnostic tumor specimens from DLBCL patients who received cyclophosphamide, adriamycin, vincristine and prednisone (CHOP)-based chemotherapy, and applied a supervised learning prediction method to identify cured vs. fatal or refractory disease. The algorithm classified two categories of patients with very different five-year overall survival rates (70% vs. 12%). The model also effectively delineated patients within specific IPI risk categories who were likely to be cured or to die of their disease. Genes implicated in DLBCL outcome included some that regulate responses to B-cell-receptor signaling, critical serine/threonine phosphorylation pathways and apoptosis. Our data indicate that supervised learning classification techniques can predict outcome in DLBCL and identify rational targets for intervention.

RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 107 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:301227 CAPLUS
DN 135:286502
TI Comparative genome-scale analysis of gene expression profiles in T cell lymphoma cells during malignant progression using a complementary DNA microarray
AU Li, Shiyong; Ross, Douglas T.; Kadin, Marshall E.; Brown, Patrick O.; Wasik, Mariusz A.
CS Department of Pathology and Laboratory Medicine, University of Pennsylvania Medical Center, Philadelphia, PA, 19104, USA
SO American Journal of Pathology (2001), 158(4), 1231-1237
CODEN: AJPAA4; ISSN: 0002-9440
PB American Society for Investigative Pathology
DT Journal

LA English
AB Using a cDNA microarray, we compared the expression of approx. 8000 genes between two unique, clonally related T cell lines derived from different stages of a progressive T cell lymphoma involving skin. A total of 180 genes was found to be differentially expressed at the RNA level by a factor of fivefold or greater. Compared with the cells from the earlier, clin. indolent stage of the lymphoma, 56 genes were up-regulated, whereas 124 genes were down-regulated in the cells from the advanced, clin. aggressive stage lymphoma. The functions of approx. 65% of these genes are currently unknown. The 22 genes with a known function that were up-regulated in the advanced lymphoma cells included several genes involved in promotion of cell proliferation and survival as well as drug resistance. The 42 functionally characterized genes that were down-regulated in the advanced lymphoma cells included neg. regulators of cell activation and cell cycle, and mediators of cell adhesion, apoptosis, and genome integrity. The differential expression identified by the cDNA microarray anal. was confirmed for selected genes by reverse transcription-polymerase chain reaction and Northern blotting. The identified differences in gene expression may be related to the differences in behavior between the early and advanced stages of the T cell lymphoma and point to directions for further investigations into mechanisms of lymphoma progression.

RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 108 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:128214 CAPLUS
DN 135:105607
TI cDNA microarray gene expression analysis of B-cell chronic lymphocytic leukemia proposes potential new prognostic markers involved in lymphocyte trafficking
AU Stratowa, Christian; Loffler, Gerald; Lichter, Peter; Stilgenbauer, Stephan; Haberl, Peter; Schweifer, Norbert; Dohner, Hartmut; Wilgenbus, Klaus K.
CS Boehringer Ingelheim Austria, Vienna, A-1121, Austria
SO International Journal of Cancer (2001), 91(4), 474-480
CODEN: IJCNAW; ISSN: 0020-7136
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Human cancer is characterized by complex mol. perturbations leading to variable clin. behavior, often even in single-disease entities. The authors performed a feasibility study systematically comparing large-scale gene expression profiles with clin. features in human B-cell chronic lymphocytic leukemia (B-CLL). CDNA microarrays were employed to determine the expression levels of 1,024 selected genes in 54 peripheral blood lymphocyte samples obtained from patients with B-CLL. Statistical analyses were applied to correlate the expression profiles with a number of clin. parameters including patient survival and disease staging. The authors were able to identify genes whose expression levels significantly correlated with patient survival and/or with clin. staging. Most of these genes code either for cell adhesion mols. (L-selectin, integrin- β 2) or for factors inducing cell adhesion mols. (IL-1 β , IL-8, EGRI), suggesting that prognosis of this disease may be related to a defect in lymphocyte trafficking. This report demonstrates the feasibility of a systematic integration of large-scale gene expression profiles with clin. data as a general approach for dissecting human diseases.

RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 109 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2001:3213 CAPLUS
DN 135:74810
TI Gene expression profiling of primary breast carcinomas using arrays of candidate genes

AU Bertucci, Francois; Houlgate, Remi; Benziane, Athmane; Granjeaud, Samuel; Adelaide, Jose; Tagett, Rebecca; Loriot, Beatrice; Jacquemier, Jocelyne; Viens, Patrice; Jordan, Bertrand; Birnbaum, Daniel; Nguyen, Catherine
CS Laboratoire de Biologie des Tumeurs, TAGC, Institut Paoli-Calmettes (IPC), Marseille, Fr.
SO Human Molecular Genetics (2000), 9(20), 2981-2991
CODEN: HMGEE5; ISSN: 0964-6906
PB Oxford University Press
DT Journal
LA English
AB Breast cancer is characterized by an important histoclin. heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. A large-scale mol. characterization of breast cancer could help in this context. Using cDNA arrays, we studied the quant. mRNA expression levels of 176 candidate genes in 34 primary breast carcinomas along three directions: comparison of tumor samples, correlations of mol. data with conventional histoclin. prognostic features and gene correlations. The study evidenced extensive heterogeneity of breast tumors at the transcriptional level. A hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clin. outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclin. parameters. No correlation was found with the age of patients, tumor size, histol. type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ($P < 0.0001$) and that of GATA3 with the presence of estrogen receptors ($P < 0.001$). Thus, our results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 96 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:818030 CAPLUS
DN 139:317418
TI Diffuse large cell lymphoma diagnosis and outcome prediction by gene expression analysis
IN Golub, Todd R.; Tamayo, Pablo; Slipp, Margaret; Lander, Eric S.; Aster, Jon C.
PA USA
SO U.S. Pat. Appl. Publ., 14 pp.
CODEN: USXXCO

DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003194701	A1	20031016	US 2001-989758	20011120
PRAI	US 2000-252142P	P	20001120		
	US 2000-254458P	P	20001208		

AB Methods for predicting phenotypic classes of lymphomas, such as lymphoma type or treatment outcome, for lymphoma samples based on gene expression profiles are described.

L5 ANSWER 88 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2004:964911 CAPLUS
DN 141:389920
TI Systems and methods for characterizing a biological condition or agent using calibrated gene expression profiles
IN Bevilacqua, Michael P.; Cheronis, John C.; Tryon, Victor; Bankaitis-Davis, Danute M.

PA USA
SO U.S. Pat. Appl. Publ., 90 pp., Cont.-in-part of U.S. Ser. No. 821,850.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 7

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2004225449	A1	20041111	US 2004-781558	20040217
	US 2003229455	A1	20031211	US 2001-821850	20010329
	US 6692916	B2	20040217		
PRAI	US 1999-141542P	P	19990628		
	US 2000-195522P	P	20000407		
	US 2000-605581	B2	20000628		
	US 2001-821850	A2	20010329		

AB Methods are provided for evaluating a biol. condition of a subject using a calibrated profile data set derived from a data set having a plurality of members, each member being a quant. measure of the amount of a subject's RNA or protein as distinct constituents in a panel of constituents. The biol. condition may be a naturally occurring physiol. state or may be responsive to treatment of the subject with one or more agents. Calibrated profile data sets may be used as a descriptive record for an agent. The index was determined with resp. to a relevant population which has in common property that is at least one of age group, gender, ethnicity, geog. location, diet, medical disorder, clin. indicator, medication, phys. activity, body mass, and environmental exposure. The biol. conditions include inflammation, diabetes, prostate health or disease, manifested skin, liver metabolism and disease, vascular disease, abnormal cell development, cancer and infectious disease. The method can be used for evaluating the effect on a biol. condition by drugs.

=> d 88 kiwc
'KIWC' IS NOT A VALID FORMAT

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=> d 88 kwic

L5 ANSWER 88 OF 111 CAPLUS COPYRIGHT 2006 ACS on STN
TI Systems and methods for characterizing a biological condition or agent using calibrated gene expression profiles
AB . . . in a panel of constituents. The biol. condition may be a naturally occurring physiol. state or may be responsive to treatment of the subject with one or more agents. Calibrated profile data sets may be used as a descriptive record for. . .
ST gene expression profiles disease diagnosis therapy surgery; system characterizing biol agent calibrated gene
9074-87-7, Folate Hydrolase 37270-94-3, Platelet factor 4 54249-88-6, Dipeptidylpeptidase IV 65802-86-0, Prostaglandin I2 synthase 79955-99-0, Matrix metalloproteinase 3 80295-33-6, Complement C1Q 80295-38-1, C-1 Esterase inhibitor 80619-02-9, Arachidonate 5-lipoxygenase 82599-72-2, Phosphatase, polynucleotide 5'-hydroxyl kinase 3'- 83869-56-1, Granulocyte-monocyte colony stimulating factor 93792-73-5, Colony stimulating factor 3 106096-93-9, Fibroblast growth factor, 2 109319-16-6 115926-52-8, Phosphoinositide-3 kinase 120178-12-3, Telomerase reverse transcriptase 122191-40-6, Caspase 1 123626-67-5, Endothelin 1 127464-60-2, Vascular endothelial growth factor 128028-50-2, Proteinase 3 133249-66-8, Proteinase inhibitor, SKALP 137632-08-7, Mitogen-activated protein kinase 1 138238-81-0, Endothelin converting enzyme 1 139639-23-9, Plasminogen activator, tissue-type 140208-23-7, PAI-1 140208-24-8, Tissue inhibitor of metalloproteinase 1 141349-86-2, Cyclin-dependent kinase 2 141436-78-4, Protein kinase C β 143180-74-9, Granzyme B 145809-21-8, Timp3 146480-35-5, Matrix Metalloproteinase 2 146480-36-6, Matrix metalloproteinase 9

146702-84-3, Mitogen activated protein kinase kinase kinase 1
147014-97-9, Cyclin-dependent kinase 4 148047-29-4, Kinase
(phosphorylating), gene TEK protein 148348-15-6, Fibroblast growth
factor 7 149885-84-7, Dual-specificity protein phosphatase
153190-38-6, Jtk14 kinase 156681-44-6, α Methylacyl-CoA racemase
157857-21-1, Maspin 169592-56-7, Caspase 3 171715-12-1, Cathepsin Z
172306-41-1, Protein kinase PCTAIRE-1 172308-17-7, Matrix
metalloproteinase 15 175449-82-8, Matrix metalloproteinase 13
180189-96-2, Caspase 9 188364-80-9, Matrix metalloproteinase 19
189460-40-0, Connective Tissue Growth Factor 214210-47-6, Neuropilin 1
241475-68-3, Metalloproteinase ADAMTS-1 245540-50-5, Proteinase MP1
289898-51-7, Mitogen activated protein kinase 8 322637-18-3, Fibroblast
growth factor 18 329736-03-0, Cytochrome P450 3A4 329764-85-4,
Cytochrome P450 1A1 329900-75-6, Prostaglandin endoperoxide synthase 2
329967-85-3, Prostaglandin endoperoxide synthase 1 330196-64-0,
Cytochrome P450 1A2 330196-93-5, Cytochrome P450 2E1 330589-90-7,
Cytochrome P450 2C19 330597-62-1, Cytochrome P450 2D6 362607-76-9,
Kallikrein 2 371761-91-0, Survivin 389069-73-2, Kallikrein 1
501433-35-8, Nitric oxide synthase 2 503473-02-7, Endothelial Nitric
oxide synthase 506430-87-1, Nitric oxide synthase 1
RL: ADV (Adverse effect, including toxicity); BSU (Biological study,
unclassified); BIOL (Biological study)

(systems and methods for characterizing a biol. condition or agent
using calibrated gene expression profiles)

IT 53-03-2, Prednisone 15687-27-1, Ibuprofen

RL: BSU (Biological study, unclassified); BIOL (Biological study)
(systems and methods for characterizing a biol. condition or agent
using calibrated gene

SYSTEM LIMITS EXCEEDED

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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	63.36	63.57
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-5.25	-5.25

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AND TECHNOLOGY CORPORATION, AND FACHINFORMATIONSZENTRUM KARLSRUHE

FILE CONTAINS CURRENT INFORMATION.

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